

GenCore version 5.1.4\_p5-4578  
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 OM protein - protein search, using sw model  
 Run on: March 13, 2003, 08:42:15 ; Search time 20.5 Seconds  
 (without alignments)  
 117.237 Million cell updates/sec  
 Title: US-09-913-524-9  
 Perfect score: 143  
 Sequence: 1 PWSPALRLRLQRPPEPSAHAFCHR 25  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*  
 2: pir2.\*  
 3: pir3.\*  
 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143	100.0	366	1 A40056	inhibin alpha chain
2	140	97.9	366	1 JC1106	inhibin alpha chain
3	131	91.6	360	1 A25732	inhibin alpha chain
4	128	89.5	366	1 A24248	inhibin alpha chain
5	127	88.8	364	1 WPCGA	inhibin alpha chain
6	89	62.2	328	2 F51215	inhibin alpha-subu
7	54	37.8	2504	1 A57788	enoyl-facyl-carrie
8	51	35.7	451	1 UBHUG	tubulin gamma chain
9	51	35.7	451	1 UBXLG	tubulin gamma chain
10	49	34.3	365	2 B83800	hypothetical prote
11	48	33.6	128	2 T44497	hypothetical prote
12	48	33.6	192	2 T09236	hypothetical prote
13	48	33.6	192	2 JC4207	nifz protein - Fra
14	47	32.9	102	2 A49361	nitrogenase Nifz c
15	47	32.9	181	2 H87577	peripherai benzodi
16	47	32.9	528	2 S35272	nitroreductase fam
17	47	32.9	577	2 T14315	dihydrofolate redu
18	47	32.9	679	2 T19703	dihydrofolate redu
19	47	32.9	2302	2 T14328	hypothetical prote
20	47	32.9	2509	2 G01880	protein-tyrosine-p
21	46.5	32.5	257	2 AH2839	fatty-acid synthas
22	46.5	32.5	257	2 B97617	conserved hypothet
23	46.5	32.5	391	2 S68354	similar to orf3 ge
24	46.5	32.5	428	2 F81660	heme d1 synthetas
25	46.5	32.5	576	2 G96763	histidyl-tRNA synt
26	46	32.2	123	2 D87587	probable WAP kinas
27	46	32.2	297	1 YXUNTP	hypothetical prote
28	46	32.2	351	2 S58192	thymidylate syntha
29	46	32.2	430	2 T36892	hypothetical prote

30 46 32.2 468 2 T50873  
 31 46 32.2 483 2 A03425  
 32 46 32.2 630 2 A36359  
 33 46 32.2 1844 1 RRPWIM  
 34 46 32.2 1844 2 S01956  
 35 46 32.2 1914 2 T42635  
 36 46 32.2 1985 2 S19151  
 37 45.5 31.8 323 2 S62085  
 38 45.5 31.8 398 2 J01245  
 39 45.5 31.8 516 2 H04424  
 40 45.5 31.8 824 2 B47301  
 41 45.5 31.8 3988 1 GNAVBV  
 42 45 31.5 63 2 I52277  
 43 45 31.5 204 2 A56671  
 44 45 31.5 356 2 E83591  
 45 45 31.5 404 2 S42578

hypothetical prote  
 xylulokinase (EC 2  
 VSG expression sit  
 genome polypeptin  
 hypothetical prote  
 tenascin Y precurs  
 hypothetical prote  
 hrpW protein - Pse  
 hypothetical 43K p  
 probable MAP kinas  
 VirB4 homolog - Bo  
 genome polypeptin  
 platelet-derived g  
 bad protein - mous  
 hypothetical prote  
 gene prune protein

#### ALIGNMENTS

##### RESULT 1

A40056

inhibin alpha chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000

C:Accession: A41398; A40056; A40905

R:Feng, Z.M.; Li, Y.P.; Chen, C.L.C.

Mol. Endocrinol. 3, 1914-1925, 1989

A:Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subun.

A:Reference number: A41398; MUID:90190649; PMID:2628729

A:Accession: A41398

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-366 <FEN>

A:Cross-references: GB:M32754; GB:M32755; NID:g204939; PIDN:AAAA1437.1; PID:g204941

R:Woodruff, T.K.; Meunier, H.; Jones, P.B.C.; Hsueh, A.J.W.; Mayo, K.E.

Mol. Endocrinol. 1, 561-568, 1987

A:Title: Rat inhibin: molecular cloning of alpha- and beta-subunit complementary de

A:Reference number: A40056; MUID:91042598; PMID:3153478

A:Accession: A40056

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-366 <MOO>

A:Cross-references: GB:M36453; NID:g204934; PIDN:AAA41435.1; PID:g204935

R:Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Uenk

Mol. Endocrinol. 1, 388-396, 1987

A:Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analys

A:Reference number: A40905; MUID:90331931; PMID:2484214

A:Accession: A40905

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-366 <ESC>

C:Suprafamily: inhibin

C:Keywords: glycoprotein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-233/Domain: propeptide #status predicted <PRO>

F:234-366/Product: inhibin alpha chain #status predicted <MAT>

F:147,269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 143; DB 1; Length 366;

Best Local Similarity 100.0%; Pred. No. 8.3e-13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PWSPALRLRLQRPPEPSAHAFCHR 25

|||||

DB 241 PWSPALRLRLQRPPEPSAHAFCHR 265

##### RESULT 2

JC1106

inhibin alpha chain precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
 C:Accession: JCI106; A60490; 148243; S31439  
 R:Su, J.G.W.; Hsueh, A.J.W.  
 Biochem. Biophys. Res. Commun. 186, 293-300, 1992  
 A>Title: Characterization of mouse inhibin alpha gene and its promoter.  
 A:Reference number: JCI106; MUID:92337610; PMID:1632772  
 A:Accession: JCI106  
 A:Molecule type: DNA  
 A:Residues: 1-164, 'R', 166-366 <SUG>  
 A:CROSS-references: GB:M95525; NID:q198404; PIDN:AAA39314.1; PID:q459875; GB:M95526  
 R:Tone, S.; Katoh, Y.; Fujimoto, H.; Toqashi, S.; Yanazawa, M.; Kato, Y.; Higashinakagawa  
 Differentiation 44, 62-68, 1990  
 A>Title: Expression of inhibin alpha-subunit gene during mouse gametogenesis.  
 A:Reference number: A60490; MUID:91071531; PMID:2253839  
 A:Accession: A60490  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 49-366 <TON>  
 A:CROSS-references: GB:X55957; NID:q296837; PIDN:CAA39424.1; PID:q296838  
 A:Experimental source: Swiss Webster  
 R:Albano, R.M.; Groome, N.; Smith, J.C.  
 Development 117, 711-723, 1993  
 A>Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells  
 A:Reference number: 148243; MUID:93321614; PMID:8330535  
 A:Accession: 148243  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-170, 'V', 172-335, 'T', 337-366 <ALB>  
 A:CROSS-references: EMBL:X9618; NID:q49936; PIDN:CAA49324.1; PID:q49937  
 C:Comment: This protein inhibits the secretion and synthesis of follicle-stimulating hor  
 C:Genetics:  
 A:Introns: 91/1  
 C:Superfamily: inhibin  
 C:Keywords: glycoprotein; gonad; heterodimer  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-233/Domain: propeptide #status predicted <PRO>  
 F:234-366/Product: inhibin alpha chain #status predicted <MAT>  
 F:147,269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.9%; Score 140; DB 1; Length 366;  
 Best Local Similarity 96.0%; Pred. No. 2.2e-12;  
 Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PWSPALRLQLRPPEPSAHAFCHR 25  
 |||||  
 Db 241 PWSPALRLQLRPPEPSAHAFCHR 265

RESULT 3  
 A25732  
 inhibin alpha chain precursor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A25732; S50897; A30161; A61548  
 R:Forage, R.G.; Ring, J.M.; Brown, R.W.; McInerney, B.V.; Cobon, G.S.; Gregson, R.P.; Ro  
 Proc. Natl. Acad. Sci. U.S.A. 83, 3091-3095, 1986  
 A>Title: Cloning and sequence analysis of cDNA species coding for the two subunits of in  
 A:Reference number: A94097; MUID:86205842; PMID:3458167  
 A:Accession: A25732  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <FOR>  
 A:CROSS-references: GB:M13273; NID:q163194; PIDN:AAA97414.1; PID:q163195  
 A>Note: part of this sequence, including the amino end of the mature protein, was confir  
 R:Thompson, D.A.; Cronin, C.N.; Martin, F.  
 Eur. J. Biochem. 226, 751-764, 1994  
 A>Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B  
 y DNase 1 footprinting.  
 A:Reference number: S50897; MUID:95112839; PMID:7813465  
 A:Accession: S50897  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-87 <THO>

A:CROSS-references: EMBL:U16237; NID:q563744; PIDN:AAB60262.1; PID:q563745  
 R:Sugino, K.; Nakamura, T.; Takio, K.; Iitani, K.; Miyamoto, K.; Hasegawa, Y.; Igara  
 Biochem. Biophys. Res. Commun. 159, 1323-1329, 1989  
 A>Title: Inhibin alpha-subunit monomer is present in bovine follicular fluid.  
 A:Reference number: A30161; MUID:89193729; PMID:2930562  
 A:Accession: A30161  
 A:Molecule type: protein  
 A:Residues: 18-37; 227-246 <SUG>  
 R:Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, K.; Mat  
 Mol. Cell. Endocrinol. 44, 55-60, 1986  
 A>Title: Isolation of bovine follicular fluid inhibin of about 32 kDa.  
 A:Reference number: A61548; MUID:86136989; PMID:3081385  
 A:Accession: A61548  
 A:Molecule type: protein  
 A:Residues: 227-230 <FUK>  
 C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.  
 C:Superfamily: inhibin  
 C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-226/Domain: propeptide #status predicted <PRO>  
 F:227-360/Product: inhibin alpha chain #status predicted <MAT>  
 F:140,262/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.6%; Score 131; DB 1; Length 360;  
 Best Local Similarity 92.0%; Pred. No. 4.3e-11;  
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PWSPALRLQLRPPEPSAHAFCHR 25  
 |||||  
 Db 234 PWSPALRLQLRPPEPSAHAFCHR 258

RESULT 4  
 A24248  
 inhibin alpha chain precursor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 01-Dec-2000  
 C:Accession: A23556; B25947; A24248  
 R:Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G.  
 FEBS Lett. 206, 329-334, 1986  
 A>Title: Human inhibin genes. Genomic characterisation and sequencing.  
 A:Reference number: A91366; MUID:87005283; PMID:3758355  
 A:Accession: A23556  
 A:Molecule type: DNA  
 A:Residues: 1-366 <STE>  
 A:CROSS-references: GB:X04445; NID:q43921; PIDN:CAA28040.1; PID:q1204105  
 R:Mayo, K.E.; Cerelli, G.M.; Spiess, J.; Rivier, J.; Rosenfeld, M.G.; Evans, R.M.; V  
 Proc. Natl. Acad. Sci. U.S.A. 83, 5849-5853, 1986  
 A>Title: Inhibin A-subunit cDNAs from porcine ovary and human placenta.  
 A:Reference number: A94116; MUID:86201450; PMID:34016724  
 A:Accession: B25947  
 A:Molecule type: mRNA  
 A:Residues: 1-366 <MAY>  
 A:CROSS-references: GB:M13981; NID:q186410; PIDN:AAA59166.1; PID:q307068  
 R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.  
 Biochem. Biophys. Res. Commun. 135, 957-964, 1986  
 A>Title: Structure of two human ovarian inhibins.  
 A:Reference number: A90123; MUID:86186863; PMID:3754442  
 A:Accession: A24248  
 A:Molecule type: mRNA  
 A:Residues: 16, 'V', 18, 'S', 20-366 <MAS>  
 A:CROSS-references: GB:M13144; NID:q186412; PIDN:AAA59167.1; PID:q186413  
 C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, resp  
 bin beta-A and beta-B, respectively.  
 C:Genetics:  
 A:Gene: GDB:INHA  
 A:CROSS-references: GDB:120100; OMIM:147380  
 A:Map position: 2q33-2q36  
 A:Introns: 90/1  
 C:Superfamily: inhibin  
 C:Keywords: glycoprotein; gonad; heterodimer; hormone  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-232/Domain: propeptide #status predicted <PRO>

```
Matches      16; Conservative      2; Mismatches      7; indels      0; Gaps      0;
```

F: 1921/Active site: lys (ol 3 oxacyl-l-acyl-carrier-protein) reductase) #status predicted  
F: 2151/Binding site: phosphopantetheine (Ser) (covalent) #status predicted  
F: 2302/Active site: Ser (ololacyl-l-acyl-carrier-protein) hydrolase #status predicted

A;Accession: A39527  
A;Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
 A:Residues: 1-451 <2HE>  
 A:Cross-references: GB:M61764; NID:g183702; PIDN:AAA52620.1; PID:g183703  
 C:Comment: This protein is a component of the centrosome that may play a role in microtubule binding.  
 C:Genetics:  
 A:Gene: GDB:TUBG  
 A:Cross-references: GDB:128600; OMIM:191135  
 A:Map position: 13q13-13q14.1  
 C:Superfamily: tubulin  
 C:Keywords: GTP binding; microtubule

Query Match 35.7%; Score 51; DB 1; Length 451;  
 Best Local Similarity 45.5%; Pred. No. 15;  
 Matches 10; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 1 PKSPAALR-LLQRPPEPSAH 20  
 II IIII I I I IIII  
 DB 350 PWGPASTQVALSRKSPYLPYSAH 371

## RESULT 9

UBXLG

tubulin gamma chain - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 22-Jun-1999  
 C:Accession: A39528  
 R:Stearns, J.; Evans, L.; Kirschner, M.

Cell 65, 825-836, 1991  
 A>Title: Gamma-tubulin is a highly conserved component of the centrosome.  
 A:Reference number: A39528; MUID:91249389; PMID:1840506  
 A:Accession: A39528

A:Molecule type: mRNA  
 A:Status: nucleic acid sequence not shown

A:Residues: 1-451 <STE>

A:Cross-references: GB:M63446; NID:g214164; PIDN:AAA49720.1; PID:g214165

C:Comment: This protein is a component of the centrosome that may play a role in microtubule binding.  
 C:Genetics:  
 A:Gene: Xqam

C:Superfamily: tubulin

C:Keywords: GTP binding; microtubule

Query Match 35.7%; Score 51; DB 1; Length 451;  
 Best Local Similarity 45.5%; Pred. No. 15;  
 Matches 10; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 1 PKSPAALR-LLQRPPEPSAH 20  
 II IIII I I I IIII  
 DB 350 PWGPASTQVALSRKSPYLPYSAH 371

## RESULT 10

FB3800

hypothetical protein BH1205 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C:Accession: FB3800

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A:Reference number: A83650; MUID:20512582; PMID:11038132

A:Accession: FB3800

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <STO>

A:Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA004924.1; GSPDB:GN00

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH1205

Query Match 34.3%; Score 49; DB 2; Length 365;  
 Best Local Similarity 61.1%; Pred. No. 24;  
 Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 WSPAALRLQLRPPEPSA 19  
 II IIII I I I  
 DB 324 WSGGLRLQLRQGESAGA 341

## RESULT 11

T44497

hypothetical protein [imported] - Thermomonospora fusca

C:Species: Thermomonospora fusca

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000

C:Accession: T44497

R:Irwin, D.I.; Zhang, S.; Wilson, D.B.

submitted to the EMBL Data Library, April 1999

A:Description: Characterization of a Thermomonospora fusca family 48 exocellulase E

A:Reference number: Z2278;

A:Accession: T44497

A:Status: preliminary; translated from GB/EMBL/UDBJ

A:Molecule type: DNA

A:Residues: 1-128 <IRW>

A:Cross-references: EMBL:AF144563; PIDN:AA039948.1

A:Experimental source: strain YX

Query Match 33.6%; Score 48; DB 2; Length 128;  
 Best Local Similarity 47.1%; Pred. No. 11;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 PAALRLQLRPPEPSAH 20  
 II IIII I I I  
 DB 18 PAGPHITQLRPHQPAAH 34

## RESULT 12

T09236

nifZ protein - Frankia alni

C:Species: Frankia alni

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: T09236

R:Benson, D.R.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z16624

A:Accession: T09236

A:Status: translated from GB/EMBL/UDBJ

A:Molecule type: DNA

A:Residues: 1-192 <BEN>

A:Cross-references: EMBL:L29299; NID:g3953454; PID:g497435

A:Experimental source: strain cp11

C:Genetics:

A:Gene: nifZ

C:Keywords: nitrogen fixation

Query Match 33.5%; Score 48; DB 2; Length 192;  
 Best Local Similarity 44.4%; Pred. No. 17;  
 Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 SPAALRLQLRPPEPSAH 20  
 IIII I I I IIII  
 DB 102 APAAVLVAEKVPAEPAH 119

## RESULT 13

JC4207

nitrogenase NifZ chain - Frankia sp.

N:Alternate names: NifZ protein

C:Species: Frankia sp.

C:Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 22-Oct-1999

C:Accession: JC4207

R:Harriott, O.T.; Hosted, T.J.; Benson, D.R.

Gene 161, 63-67, 1995

A>Title: Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia nitrogen fi

A:Reference number: JC4203; MUID:95369734; PMID:7642138

A:Accession: JC4207

A:Molecule type: DNA

A:Residues: 1-192 <HAR>

A:Cross-references: GB:L29299; NID:g497430; PIDN:AAC82974.1; PID:g497435  
 C:Comment: This protein has an Ala and Pro rich region at its carboxyl-terminal region.  
 C:Genetics:  
 A:Gene: nifZ  
 C:Keywords: nitrogen fixation

Query Match 33.6%; Score 48; DB 2; Length 192;  
 Best Local Similarity 44.4%; Pred. No. 17;  
 Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 SPAALRLQRPPEPSAH 20  
 :||| : : : ||||  
 Db 102 APAAVLVAEKVPAEPAAH 119

## RESULT 14

A49361  
 peripheral benzodiazepine receptor-related protein - human  
 C:Species: Homo sapiens (man)  
 C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999  
 C:Accession: A49361  
 R:Lin, D.; Chang, Y.J.; Strauss, J.P.; Miller, W.L.  
 Genomics 18, 643-650, 1993  
 A:Title: The human peripheral benzodiazepine receptor gene: cloning and characterization  
 A:Reference number: A49361; MUID:94140364; PMID:8307574  
 A:Accession: A49361  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-102 <RES>  
 A:Cross-references: GB:L21950; NID:g483401; PIDN:AAA18227.1; PID:g488420

Query Match 32.9%; Score 47; DB 2; Length 102;  
 Best Local Similarity 39.1%; Pred. No. 12;  
 Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 WSPAALRLQRPPEPSAHAFCH 24  
 :||| : || : || : ||  
 Db 59 WGTAAARVSARETRDCSTSRCH 91

## RESULT 15

I187577  
 nitroreductase family protein [imported] - Caulobacter crescentus  
 C:Species: Caulobacter crescentus  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 03-Jun-2002  
 C:Accession: I187577  
 R:Kierman, W.C.; Feidolyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 B.; Lauth, M.T.; Dekey, R.L.; Dodson, R.J.; Dukin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A:Title: Complete Genome Sequence of Caulobacter crescentus.  
 A:Reference number: I187577; MUID:21173698; PMID:11259647  
 A:Accession: I187577  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-181 <STO>  
 A:Cross-references: GB:AE005673; NID:g13424234; PIDN:AAK24620.1; GSPDB:GN00148  
 C:Genetics:  
 A:Gene: CC2653  
 C:Superfamily: Methanobacterium thermoautotrophicum NADPH-oxidoreductase

Query Match 32.9%; Score 47; DB 2; Length 181;  
 Best Local Similarity 33.3%; Pred. No. 22;  
 Matches 13; Conservative 2; Mismatches 6; Indels 18; Gaps 1;

QY 5 AALRLQRPPEPSAHAFCH 25  
 :||| : || : || : ||  
 Db 76 AALRLQRPPEPSAHAFCH 114

Search completed: March 13, 2003, 13:59:34  
 Job Time : 21.5 secs